



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: SHERMAN, Linda A.  
LUSTGARTEN, Joseph
- (ii) TITLE OF THE INVENTION: RECOMBINANT CONSTRUCTS ENCODING  
T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR  
ANTIGENS
- (iii) NUMBER OF SEQUENCES: 64
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20006-1888
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/812,393  
(B) FILING DATE: 05-MAR-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Murashige, Kate H  
(B) REGISTRATION NUMBER: 29,959  
(C) REFERENCE/DOCKET NUMBER: 31333-20001.00
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-887-1500  
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1350 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ix) FEATURE:  
(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...1332  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val 1 5 10 15	48
CAG ATT TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC Gln Ile Cys Trp Leu Lys Glu Gln Val Gln Gln Ser Pro Ala Ser 20 25 30	96
TTG GTT CTG CAG GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser 35 40 45	144
ATC TTT ACA AAC CAG GTG CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg 50 55 60	192
CTC GTC AGC CTG TTG TAC AAT CCT TCT GGG ACA AAG CAG AGT GGG AGA Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg 65 70 75 80	240
CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT CGC AGC TCT TTG CAC ATT Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile 85 90 95	288
TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC TGT GCC TCA AAT Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn 100 105 110	336
TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT AAA CTC Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu 115 120 125	384
TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly 130 135 140	432
GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala 145 150 155 160	480
GTA ACA GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His 165 170 175	528
AAC AAC ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu 180 185 190	576
ATC CAT TAT TCA TAT GGT GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro 195 200 205	624
GAT GGA TAC AAG GCC TCC AGA CCA AGC CAA GAG AAC TTC TCC CTC ATT Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile 210 215 220	672
CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA GTG TAC TTC TGT GCC AGC Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser 225 230 235 240	720

GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT CAT GGA ACC AAG Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys 245 250 255	768
CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC TTC GTG Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val 260 265 270	816
CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro 275 280 285	864
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro 290 295 300	912
TCT AGT TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu 305 310 315 320	960
TTC ATC TAT GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe 325 330 335	1008
AGC AGG AGC GCA GAC GCC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu 340 345 350	1056
TAT AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp 355 360 365	1104
AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG GGA AAG CCG AGA AGG AAG Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys 370 375 380	1152
AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala 385 390 395 400	1200
GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG GGC AAG Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys 405 410 415	1248
GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr 420 425 430	1296
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAAGCGGCCG CCACCG Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg 435 440	1348
CG	1350

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 444 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val  
 1 5 10 15  
 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser  
 20 25 30  
 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser  
 35 40 45  
 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg  
 50 55 60  
 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg  
 65 70 75 80  
 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile  
 85 90 95  
 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn  
 100 105 110  
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu  
 115 120 125  
 Ser Val Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
 130 135 140  
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala  
 145 150 155 160  
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His  
 165 170 175  
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu  
 180 185 190  
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro  
 195 200 205  
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile  
 210 215 220  
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser  
 225 230 235 240  
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Gly His Gly Thr Lys  
 245 250 255  
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val  
 260 265 270  
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro  
 275 280 285  
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro  
 290 295 300  
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu  
 305 310 315 320  
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe  
 325 330 335  
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu  
 340 345 350  
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
 355 360 365  
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
 370 375 380  
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
 385 390 395 400  
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys  
 405 410 415  
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr  
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
435 440

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCAAGGCAC TGATGTTTCAT CTC

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGAGACAAAG TCCCCAATCT CTGACAG

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGCTGC TCCTCAAGTA CTATTC

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-4.1.2.3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCCGGAGAA GGTCCACAGT TCCTCTTT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-4.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCAGCAG AGGGTTTGAA GCCACATAC

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGGTCTT CAGTTGCTTA TGAAGGT

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTTCCTCTT CAGGGTCCAG AATATGT

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAAGAAGT CACCCTGGAC TGTTTCAT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCTCCACA GACAACAAGA GGACCGAGCA

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGCTGCGAC GTTCCTTAGT GACTGTG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGTCAGC CTGTTGTCCA ATCCTTCTGG

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGCCTCATC AATCTGTTCT ACTTGGCT

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCAGGGA CCACAGTTTA TCATTCAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCTGGAGAG AATCCTAAGC TCATCAT

27

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCTTG TG TCCCTGACAG TCCTGGTT

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-16



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAAGCAAACA CTGTAGTGCA GAGCCCTTCC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGACATCC ATAAGTGCCC TACAG

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTGTATGAAA CCCAGGACAG TTCTTAC

27

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGTATTTCT TTCTTATGTT GTTTTGAT

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-alpha-20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAAAGCTCTC CATCGCTGAC TGTTCAAG

28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATCTAATCCT GGGAAGAGCA AAT

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCGTCTGGT ACCACGTGGT CAA

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGAAAGGCC AAGGACAAAA AGC

23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATGCGAA CAGTATCTAG GC

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-5.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACATAATCAA AGGAAAGGGA GAA

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCCTGATTGG TCAGGAAGGG CAA

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TACCTGATCA AAAGAATGGG AGA

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-8.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAACCATGA CAATATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-8.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAACCACAA CAACATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-8.3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGCCACAA CTACATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCTTGCAAG AGTTGGA AAAA CCA

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATTATGTTT AGCTACAATA ATA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACAAGGTGAC AGGGAAGGGA CAA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACCTACAGAA CCCAAGGACT CAG

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGTTGCCCT CGGATCGATT TTC

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCCGAGATCA AGGCTGTGGG CAG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGAACCATCT GTAAGAGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CATCAAATAA TAGATATGGG GCA

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTAGTCCTGA AAAAGGGCAC ACT

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) ISOLATE: V-beta-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CATCTGTCAA AGTGGCACTT CA

22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...393
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTG TGG CTC CAG TTA AAC 48  
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn  
1 5 10 15

TGG GTG CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT 96  
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser  
20 25 30

GTC CCA GAG GGA GGC ATG GCC TCT CTC AAC TGC ACT TCA AGT GAT CGC 144  
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg  
35 40 45

AAT TTT CAG TAT TTC TGG TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC 192  
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro  
50 55 60

AAA GCA CTG ATG TCC ATC TTC TCT GAT GGT GAC AAG AAA GAA GGC AGA 240  
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg  
65 70 75 80

TTC ACA GCT CAC CTC AAT AAG GCC AGC CTG CAT GTT TCC CTG CAC ATC 288  
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile  
85 90 95

AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC TGT GCA GTT ATG 336  
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met  
100 105 110

GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG TTA TCT 384  
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser  
115 120 125

ATC AAG CCC 393  
Ile Lys Pro  
130

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn  
1 5 10 15  
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser  
20 25 30  
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg  
35 40 45  
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro  
50 55 60  
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg  
65 70 75 80  
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile  
85 90 95  
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met  
100 105 110  
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser  
115 120 125  
Ile Lys Pro  
130

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...402  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA 48  
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys  
1 5 10 15  
CAC ATG GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA 96  
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val  
20 25 30  
ACA GGA GGA AAG GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC 144  
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp  
35 40 45  
TAT ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC 192  
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile  
50 55 60



CAT TAC TCA TAT GTC GCT GAC AGC ACG GAG AAA GGA GAT ATC CCT GAT	240
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp	
65 70 75 80	
GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG AAT TTC TCT CTC ATT CTG	288
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu	
85 90 95	
GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC TGT GCG AGC AGC	336
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser	
100 105 110	
GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT CCC GGC	384
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly	
115 120 125	
ACC AGG CTC ACG GTT TCT	402
Thr Arg Leu Thr Val Ser	
130	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys	
1 5 10 15	
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val	
20 25 30	
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp	
35 40 45	
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile	
50 55 60	
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp	
65 70 75 80	
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu	
85 90 95	
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser	
100 105 110	
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly	
115 120 125	
Thr Arg Leu Thr Val Ser	
130	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ile Phe Gly Ser Leu Ala Phe Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Met Ala Gly Val Gly Ser Pro Tyr Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Leu Tyr Gln Gly Gln Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Leu Leu Gln Glu Thr Glu Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Ile Pro Val Ala Ile Lys Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Cys Leu Thr Ser Thr Val Gln Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Leu Met Pro Tyr Gly Cys Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Val Leu Val Lys Ser Pro Asn His Val  
1 5

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asp Ile Asp Glu Thr Glu Tyr His Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Leu Leu Glu Lys Gly Glu Arg Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Leu Val Ser Glu Phe Ser Arg Met  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Glu Leu Val Ser Glu Phe Ser Arg Met Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Val Ser Glu Phe Ser Arg Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Leu Val Asp Ala Glu Glu Tyr Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Leu Ser Pro Gly Lys Asn Gly Val  
1 5

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Lys Leu Val Gly Lys Leu Asn Trp Ala  
1 5